

segments which are substantially complementary to nucleic acid segments that flank and/or extend partially or fully across breakpoint regions known to be associated with genetic translocations, wherein each probe comprises a distinct fluorescent label;

(b) reacting the heterogeneous mixture with the targeted chromosomal DNA by in situ hybridization; and

(c) observing the proximity or overlap of the regions stained by each probe, to determine whether said translocation is present in the interphase cell.

*1*  
*Conf*  
<sup>28</sup>  
~~163~~. The method according to claim ~~131~~<sup>1</sup>, wherein said probes have a combined complexity of between about 50 kb and 750 kb.

<sup>29</sup>  
~~164~~. A method of distinguishing normal and malignant cells comprising staining target chromosomal DNA to detect in an interphase cell one or more genetic translocations identified with chromosomal abnormalities of malignant cells, said method comprising:

(a) providing a heterogeneous mixture of two or more nucleic acid probes having a combined complexity of about 50 kb, which probes contain nucleic acid segments which are substantially complementary to nucleic acid segments that flank and/or extend partially or fully across breakpoint regions known to be associated

with genetic translocations, wherein each probe comprises a distinct fluorescent label;

(b) reacting the heterogeneous mixture with the targeted chromosomal DNA by in situ hybridization;

(c) observing the proximity or overlap of the regions stained by each probe to determine whether said translocation is present in the interphase cell, wherein said translocation is indicative of a malignant cell.

<sup>30</sup>  
~~105~~. A method of determining prognosis for a patient and/or determining the effectiveness of a therapy comprising staining target chromosomal DNA to detect in an interphase cell one or more genetic translocations identified with chromosomal abnormalities of malignant cells, said method comprising:

(a) providing a heterogeneous mixture of two or more nucleic acid probes having a combined complexity of about 50 kb, which probes contain nucleic acid segments which are substantially complementary to nucleic acid segments that flank and/or extend partially or fully across breakpoint regions known to be associated with genetic translocations, wherein each probe comprises a distinct fluorescent label;

(b) reacting the heterogeneous mixture with the targeted chromosomal DNA by in situ hybridization;

(c) observing the proximity or overlap of the regions stained by each probe to determine whether said translocation is present in the interphase cell, wherein the occurrence of a translocation is indicative of the prognosis of the patient and/or the effectiveness of therapy.

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~~166.~~ (Amended) A method of staining target chromosomal DNA to detect in an interphase cell one or more genetic translocations identified with chromosomal abnormalities, said method comprising:

(a) providing a heterogeneous mixture of two or more nucleic acid probes having a combined complexity of about 50 kb, which probes contain nucleic acid segments which are substantially complementary to nucleic acid segments that flank and/or extend partially or fully across breakpoint regions known to be associated with genetic translocations;

(b) reacting the heterogeneous mixture with the targeted chromosomal DNA by in situ hybridization;

(c) adding a distinct fluorescent label to each of said nucleic acid probes;  
and

(d) observing the proximity or overlap of the regions stained by each probe, to determine whether said translocation is present in the interphase cell.